

SEQUENCE LISTING

<110> Gregory, Richard L.

<120> Methods and Compositions for Controlling Dental Caries,
and Recombinant SmaA Polypeptides Useful for Same

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<150> 60/132,312

<151> 1999-05-03

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<170> PatentIn Ver. 2.1

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Met	Asn	Gln	Lys	Ile	Val
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Val	Ile	Ser	Ser	Phe	Tyr	Met	Leu	Gly	Ala	His	Ser	Phe	Ser	Lys	Ala	
10							15						20			

gta	tat	cat	aat	gat	agg	agt	gtg	aaa	ctt	atg	aaa	aga	att	gat	att	929
Val	Tyr	His	Asn	Asp	Arg	Ser	Val	Lys	Leu	Met	Lys	Arg	Ile	Asp	Ile	
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Asn	His	Gln	Ala	Gln	Arg	Phe	Ser	Ile	Arg	Lys	Tyr	Ala	Phe	Gly	Ala	
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gca	tct	gtt	tta	att	ggc	tgt	gtc	ttt	ttt	cta	ggt	acc	caa	aat	gtt	1025
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Ser	Ala	Gln	Glu	Gln	Gly	Thr	Gln	Leu	Pro	Ala	Ser	Glu	Asn	Ala	Val	
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gtg	aac	gtg	gct	gaa	aat	tca	gtt	gct	atc	agc	caa	gca	gtt	gca	gat	1121
Val	Asn	Val	Ala	Glu	Asn	Ser	Val	Ala	Ile	Ser	Gln	Ala	Val	Ala	Asp	
90							95						100			

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Lys	Ala	Ala	Thr	Gln	Thr	Thr	Leu	Thr	Glu	Thr	Pro	Gln	Val	Glu	Val	
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gag	gag	aaa	gaa	agt	aag	gtt	aat	gct	cct	gct	tta	aat	gtc	gat	gac	1217
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aaa	ggt	gca	aaa	tcc	aaa	gaa	gat	gtg	aac	cct	act	att	tca	aag	aca	1265
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Ala	Ser	Glu	Val	Glu	Ala	Ser	Ala	Val	Thr	Ala	Thr	Asp	Thr	Lys	Asn	
155							160						165			

tca	aat	cca	caa	gtc	aat	gtt	gaa	act	gac	tca	agt	gaa	aaa	gac	gaa	1361
Ser	Asn	Pro	Gln	Val	Asn	Val	Glu	Thr	Asp	Ser	Ser	Glu	Lys	Asp	Glu	
170							175						180			

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Val Ser Ile Pro Ser Gln Gly Asn Tyr Val Phe Gln Glu Thr Thr Pro			
215	220	225	230
gta aaa aat gca gcc agt atg tcc agc cca acc caa ttt aac ttt gat			1553
Val Lys Asn Ala Ala Ser Met Ser Pro Thr Gln Phe Asn Phe Asp			
235	240	245	
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Lys Gly Asp Lys Val Phe Tyr Asp Asn Val Leu Glu Ala Asp Gly His			
250	255	260	
caa tgg att agc tat gtg tct tac agt ggt att cgt cgc tat gct cct			1649
Gln Trp Ile Ser Tyr Val Ser Tyr Ser Gly Ile Arg Arg Tyr Ala Pro			
265	270	275	
att gct gtg aca att gaa gaa ttg aag caa aaa gaa att gtt cag caa			1697
Ile Ala Val Thr Ile Glu Glu Leu Lys Gln Lys Glu Ile Val Gln Gln			
280	285	290	
aat tta ccg gca caa gga acc tat cac ttt act aaa cag cag agc tta			1745
Asn Leu Pro Ala Gln Gly Thr Tyr His Phe Thr Lys Gln Gln Ser Leu			
295	300	305	310
aaa atg aag cta aac tgt cta gtc cga ccc aat tct cgt ttt aca acg			1793
Lys Met Lys Leu Asn Cys Leu Val Arg Pro Asn Ser Arg Phe Thr Thr			
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gag acc acg ttt ttt atg ata agg ttt tagaagcgga tggacatcaa			1840
Glu Ile Thr Phe Phe Met Ile Arg Phe			
330	335		
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Lys Tyr Ala Phe Gly Ala Ala Ser Val Leu Ile Gly Cys Val Phe Phe

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Phe	Gln	Glu	Thr	Thr	Pro	Val	Lys	Asn	Ala	Ala	Ser	Met	Ser	Ser	Pro
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Thr	Gln	Phe	Asn	Phe	Asp	Lys	Gly	Asp	Lys	Val	Phe	Tyr	Asp	Asn	Val
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Leu	Glu	Ala	Asp	Gly	His	Gln	Trp	Ile	Ser	Tyr	Val	Ser	Tyr	Ser	Gly
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Ile	Arg	Arg	Tyr	Ala	Pro	Ile	Ala	Val	Thr	Ile	Glu	Glu	Leu	Lys	Gln
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Lys	Glu	Ile	Val	Gln	Gln	Asn	Leu	Pro	Ala	Gln	Gly	Thr	Tyr	His	Phe
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Thr	Lys	Gln	Gln	Ser	Leu	Lys	Met	Lys	Leu	Asn	Cys	Leu	Val	Arg	Pro

305

310

315

320

Asn Ser Arg Phe Thr Thr Glu Ile Thr Phe Phe Met Ile Arg Phe
325 330 335